

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/466,343DDATE: 12/10/98
TIME: 14:56:45

INPUT SET: S30278.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information:
4
5 (i) APPLICANT: LI, Yi
6
7 (ii) TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN
8 CHEMOKINE RECEPTOR HDG NR10 (AS AMENDED)
9
10 (iii) NUMBER OF SEQUENCES: 9
11
12 (iv) CORRESPONDENCE ADDRESS:
13 (A) ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
14 (B) STREET: 1100 NEW YORK AVE., NW, SUITE 600
15 (C) CITY: WASHINGTON
16 (D) STATE: DC
17 (E) COUNTRY: USA
18 (F) ZIP: 20005
19
20 (v) COMPUTER READABLE FORM:
21 (A) MEDIUM TYPE: Floppy disk
22 (B) COMPUTER: IBM PC compatible
23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
25
26 (vi) CURRENT APPLICATION DATA:
27 (A) APPLICATION NUMBER: US 08/466,343
28 (B) FILING DATE: 06-JUN-1995
29 (C) CLASSIFICATION:
30
31 (viii) ATTORNEY/AGENT INFORMATION:
32 (A) NAME: STEFFE, ERIC K.
33 (B) REGISTRATION NUMBER: 36,688
34 (C) REFERENCE/DOCKET NUMBER: 1488.1150000/EKS/KLM
35
36 (ix) TELECOMMUNICATION INFORMATION:
37 (A) TELEPHONE: (202) 371-2600
38 (B) TELEFAX: (202) 371-2540
39
40
41 (2) INFORMATION FOR SEQ ID NO:1:
42
43 (i) SEQUENCE CHARACTERISTICS:
44 (A) LENGTH: 1414 base pairs
45 (B) TYPE: nucleic acid
46 (C) STRANDEDNESS: double

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47 (D) TOPOLOGY: linear
48
49 (ii) MOLECULE TYPE: cDNA
50
51
52 (ix) FEATURE:
53 (A) NAME/KEY: CDS
54 (B) LOCATION: 259..1314
55
56
57 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
58
59 GTGAGATGGT GCTTTCATGA ATTCCCCCAA CAAGAGCCAA GCTCTCCATC TAGTGGACAG 60
60
61 GGAAGCTAGC AGCAAACCTT CCCTTCACTA CGAAACTTCA TTGCTTGGCC CAAAAGAGAG 120
62
63 TTAATTCAAT GTAGACATCT ATGTAGGCAA TTAAAAACCT ATTGATGTAT AAAACAGTTT 180
64
65 GCATTCATGG AGGGCAACTA AATACATTCT AGGACTTTAT AAAAGATCAC TTTTATTATTA 240
66
67 TGCACAGGGT GGAACAAG ATG GAT TAT CAA GTG TCA AGT CCA ATC TAT GAC 291
68 Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp
69 1 5 10
70
71 ATC AAT TAT TAT ACA TCG GAG CCC TGC CCA AAA ATC AAT GTG AAG CAA 339
72 Ile Asn Tyr Tyr Thr Ser Glu Pro Cys Pro Lys Ile Asn Val Lys Gln
73 15 20 25
74
75 ATC GCA GCC CGC CTC CTG CCT CCG CTC TAC TCA CTG GTG TTC ATC TTT 387
76 Ile Ala Ala Arg Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe
77 30 35 40
78
79 GGT TTT GTG GGC AAC ATG CTG GTC ATC CTC ATC CTG ATA AAC TGC CAA 435
80 Gly Phe Val Gly Asn Met Leu Val Ile Leu Ile Leu Ile Asn Cys Gln
81 45 50 55
82
83 AGG CTG GAG AGC ATG ACT GAC ATC TAC CTG CTC AAC CTG GCC ATC TCT 483
84 Arg Leu Glu Ser Met Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser
85 60 65 70 75
86
87 GAC CTG TTT TTC CTT CTT ACT GTC CCC TTC TGG GCT CAC TAT GCT GCC 531
88 Asp Leu Phe Phe Leu Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala
89 80 85 90
90
91 GCC CAG TGG GAC TTT GGA AAT ACA ATG TGT CAA CTC TTG ACA GGG CTC 579
92 Ala Gln Trp Asp Phe Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu
93 95 100 105
94
95 TAT TTT ATA GGC TTC TTC TCT GGA ATC TTC TTC ATC ATC CTC CTG ACA 627
96 Tyr Phe Ile Gly Phe Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr
97 110 115 120
98
99 ATC GAT AGG TAC CTG GCT ATC GTC CAT GCT GTG TTT GCT TTA AAA GCC 675

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| 100 | Ile | Asp | Arg | Tyr | Leu | Ala | Ile | Val | His | Ala | Val | Phe | Ala | Leu | Lys | Ala | |
| 101 | | 125 | | | | | 130 | | | | | 135 | | | | | |
| 102 | | | | | | | | | | | | | | | | | |
| 103 | AGG | ACG | GTC | ACC | TTT | GGG | GTG | GTG | ACA | AGT | GTG | ATC | ACT | TGG | GTG | GTG | 723 |
| 104 | Arg | Thr | Val | Thr | Phe | Gly | Val | Val | Thr | Ser | Val | Ile | Thr | Trp | Val | Val | |
| 105 | 140 | | | | | 145 | | | | | 150 | | | | | 155 | |
| 106 | | | | | | | | | | | | | | | | | |
| 107 | GCT | GTG | TTT | GCG | TCT | CTC | CCA | GGA | ATC | ATC | TTT | ACC | AGA | TCT | CAA | AAA | 771 |
| 108 | Ala | Val | Phe | Ala | Ser | Leu | Pro | Gly | Ile | Ile | Phe | Thr | Arg | Ser | Gln | Lys | |
| 109 | | | | | 160 | | | | | 165 | | | | | | 170 | |
| 110 | | | | | | | | | | | | | | | | | |
| 111 | GAA | GGT | CTT | CAT | TAC | ACC | TGC | AGC | TCT | CAT | TTT | CCA | TAC | AGT | CAG | TAT | 819 |
| 112 | Glu | Gly | Leu | His | Tyr | Thr | Cys | Ser | Ser | His | Phe | Pro | Tyr | Ser | Gln | Tyr | |
| 113 | | | | 175 | | | | | 180 | | | | | 185 | | | |
| 114 | | | | | | | | | | | | | | | | | |
| 115 | CAA | TTC | TGG | AAG | AAT | TTC | CAG | ACA | TTA | AAG | ATA | GTC | ATC | TTG | GGG | CTG | 867 |
| 116 | Gln | Phe | Trp | Lys | Asn | Phe | Gln | Thr | Leu | Lys | Ile | Val | Ile | Leu | Gly | Leu | |
| 117 | | | 190 | | | | | 195 | | | | | 200 | | | | |
| 118 | | | | | | | | | | | | | | | | | |
| 119 | GTC | CTG | CCG | CTG | CTT | GTC | ATG | GTC | ATC | TGC | TAC | TCG | GGA | ATC | CTA | AAA | 915 |
| 120 | Val | Leu | Pro | Leu | Leu | Val | Met | Val | Ile | Cys | Tyr | Ser | Gly | Ile | Leu | Lys | |
| 121 | | | 205 | | | | 210 | | | | | | 215 | | | | |
| 122 | | | | | | | | | | | | | | | | | |
| 123 | ACT | CTG | CTT | CGG | TGT | CGA | AAT | GAG | AAG | AAG | AGG | CAC | AGG | GCT | GTG | AGG | 963 |
| 124 | Thr | Leu | Leu | Arg | Cys | Arg | Asn | Glu | Lys | Lys | Arg | His | Arg | Ala | Val | Arg | |
| 125 | 220 | | | | | 225 | | | | | 230 | | | | | 235 | |
| 126 | | | | | | | | | | | | | | | | | |
| 127 | CTT | ATC | TTC | ACC | ATC | ATG | ATT | GTT | TAT | TTT | CTC | TTC | TGG | GCT | CCC | TAC | 1011 |
| 128 | Leu | Ile | Phe | Thr | Ile | Met | Ile | Val | Tyr | Phe | Leu | Phe | Trp | Ala | Pro | Tyr | |
| 129 | | | | | 240 | | | | | 245 | | | | | 250 | | |
| 130 | | | | | | | | | | | | | | | | | |
| 131 | AAC | ATT | GTC | CTT | CTC | CTG | AAC | ACC | TTC | CAG | GAA | TTC | TTT | GGC | CTG | AAT | 1059 |
| 132 | Asn | Ile | Val | Leu | Leu | Asn | Thr | Phe | Gln | Glu | Phe | Phe | Phe | Gly | Leu | Asn | |
| 133 | | | | 255 | | | | | 260 | | | | | 265 | | | |
| 134 | | | | | | | | | | | | | | | | | |
| 135 | AAT | TGC | AGT | AGC | TCT | AAC | AGG | TTG | GAC | CAA | GCT | ATG | CAG | GTG | ACA | GAG | 1107 |
| 136 | Asn | Cys | Ser | Ser | Ser | Asn | Arg | Leu | Asp | Gln | Ala | Met | Gln | Val | Thr | Glu | |
| 137 | | | 270 | | | | | 275 | | | | | 280 | | | | |
| 138 | | | | | | | | | | | | | | | | | |
| 139 | ACT | CTT | GGG | ATG | ACG | CAC | TGC | TGC | ATC | AAC | CCC | ATC | ATC | TAT | GCC | TTT | 1155 |
| 140 | Thr | Leu | Gly | Met | Thr | His | Cys | Cys | Ile | Asn | Pro | Ile | Ile | Tyr | Ala | Phe | |
| 141 | | | 285 | | | | 290 | | | | | 295 | | | | | |
| 142 | | | | | | | | | | | | | | | | | |
| 143 | GTC | GGG | GAG | AAG | TTC | AGA | AAC | TAC | CTC | TTA | GTC | TTC | TTC | CAA | AAG | CAC | 1203 |
| 144 | Val | Gly | Glu | Lys | Phe | Arg | Asn | Tyr | Leu | Leu | Val | Phe | Phe | Gln | Lys | His | |
| 145 | 300 | | | | | 305 | | | | | 310 | | | | | 315 | |
| 146 | | | | | | | | | | | | | | | | | |
| 147 | ATT | GCC | AAA | CGC | TTC | TGC | AAA | TGC | TGT | TCT | ATT | TTC | CAG | CAA | GAG | GCT | 1251 |
| 148 | Ile | Ala | Lys | Arg | Phe | Cys | Lys | Cys | Cys | Ser | Ile | Phe | Gln | Gln | Glu | Ala | |
| 149 | | | | | 320 | | | | | 325 | | | | | 330 | | |
| 150 | | | | | | | | | | | | | | | | | |
| 151 | CCC | GAG | CGA | GCA | AGC | TCA | GTT | TAC | ACC | CGA | TCC | ACT | GGG | GAG | CAG | GAA | 1299 |
| 152 | Pro | Glu | Arg | Ala | Ser | Ser | Val | Tyr | Thr | Arg | Ser | Thr | Gly | Glu | Gln | Glu | |

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153          335          340          345
154
155  ATA TCT GTG GGC TTG TGACACGGAC TCAAGTGGGC TGGTGACCCA GTCAGAGTTG      1354
156  Ile Ser Val Gly Leu
157          350
158
159  TGCACATGGC TTAGTTTTCA TACACAGCCT GGGCTGGGGG TGGGGTGGAA GAGGTCTTTT      1414
160
161
162
163  (2) INFORMATION FOR SEQ ID NO:2:
164
165      (i) SEQUENCE CHARACTERISTICS:
166          (A) LENGTH: 352 amino acids
167          (B) TYPE: amino acid
168          (D) TOPOLOGY: linear
169
170      (ii) MOLECULE TYPE: protein
171
172      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
173
174  Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr
175      1          5          10          15
176
177  Ser Glu Pro Cys Pro Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu
178          20          25          30
179
180  Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn
181          35          40          45
182
183  Met Leu Val Ile Leu Ile Leu Ile Asn Cys Gln Arg Leu Glu Ser Met
184          50          55          60
185
186  Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu
187          65          70          75          80
188
189  Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe
190          85          90          95
191
192  Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe
193          100         105         110
194
195  Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu
196          115         120         125
197
198  Ala Ile Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe
199          130         135         140
200
201  Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser
202          145         150         155         160
203
204  Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr
205          165         170         175

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206
207 Thr Cys Ser Ser His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn
208 180 185 190
209
210 Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu Val Leu Pro Leu Leu
211 195 200 205
212
213 Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys
214 210 215 220
215
216 Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg Leu Ile Phe Thr Ile
217 225 230 235 240
218
219 Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr Asn Ile Val Leu Leu
220 245 250 255
221
222 Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser Ser
223 260 265 270
224
225 Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu Thr Leu Gly Met Thr
226 275 280 285
227
228 His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe
229 290 295 300
230
231 Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His Ile Ala Lys Arg Phe
232 305 310 315 320
233
234 Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala Pro Glu Arg Ala Ser
235 325 330 335
236
237 Ser Val Tyr Thr Arg Ser Thr Gly Glu Gln Glu Ile Ser Val Gly Leu
238 340 345 350
239

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 BASE PAIRS

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGGAATTCCT CCATGGATTA TCAAGTGTCA

30

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 BASE PAIRS

PAGE: 1

SEQUENCE VERIFICATION REPORT
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Line

Error

Original Text